

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

Structure of the PCA3 transcription unit

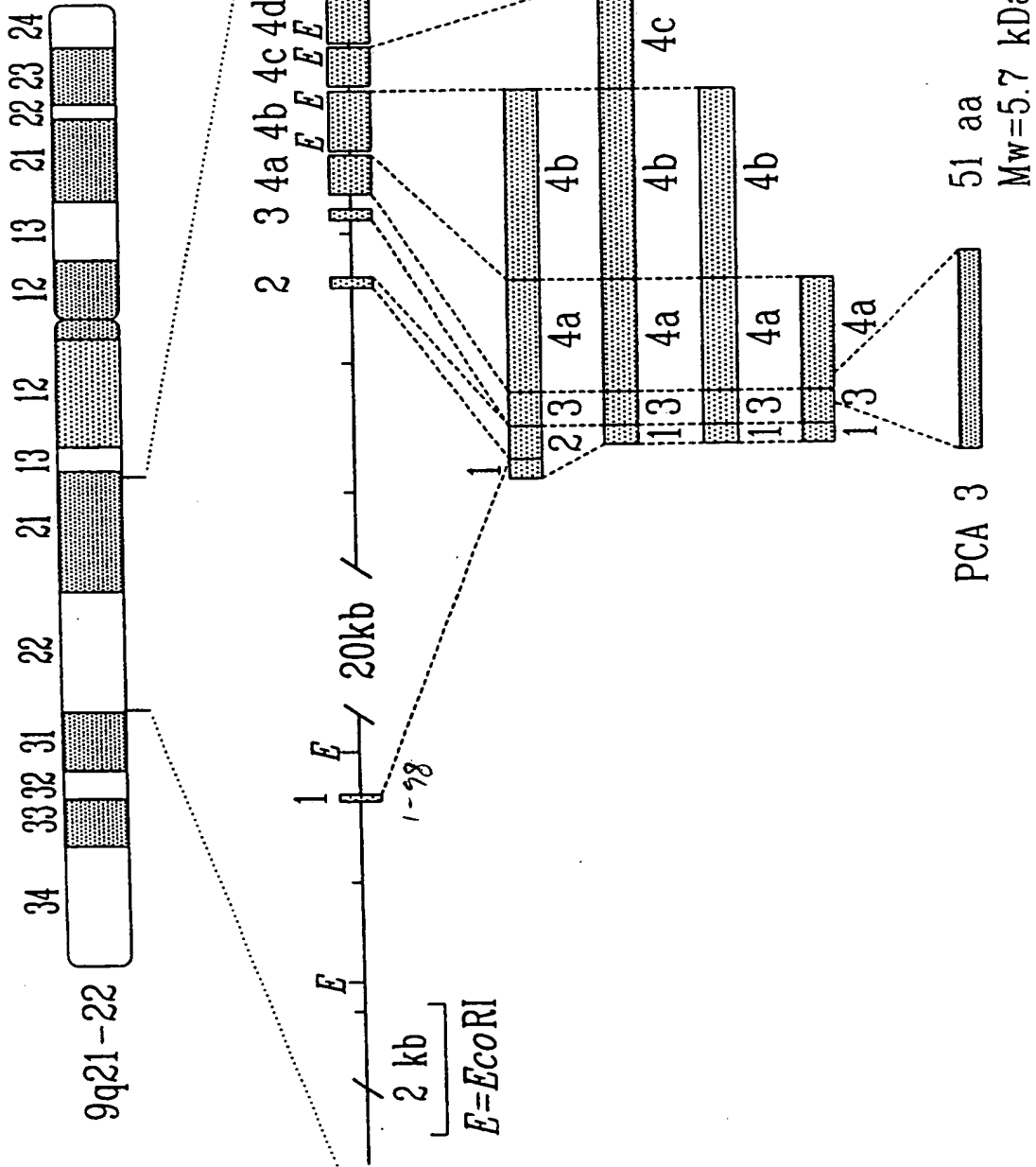


FIG. 1

APPROVED	O.G. FIG.	
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[illegible]

379 531

1	99	264	447	986	
1	98	263	446	985	2037

>---PCA3--->

>-EXON1->-----EXON2----->-----EXON3-----EXON4a-----EXON4b----->
 1 |-----EXON2-----EXON3-----EXON4a-----EXON4b----->
 1 |-----EXON2-----EXON3-----EXON4a-----EXON4b----->

711-22A

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1) EXON1, 2) EXON2, 3) EXON3, 4) EXON4A, 5) EXON4b, PCA3 (amino acids)
(poly-A-addition signals are underlined)
CON) : Range= 1 to 2037

Name Base

1 1 agaagctggc atcagaaaaa cagagggggag atttgtgtgg ctgcagccga gggagaccag

CON 1 AGAAGCTGGC ATCAGAAAAA CAGAGGGGAG ATTTGTGTGG CTGCAGCCGA GGGAGACCAG

1 1 gaagatctgc atggtggga ggacctgatg atacagag
61

ga attacaacac atatacttag

First 2B

APPROVED	O.G. FIG.	
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CON 300 AGGCCACACA TCTGCTGAA TGGAGATAAT TAACATCACT AGAAACAGCA AGATGACAAAT

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[illegible]

APPROVED	O.G. FIG.	
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3 97 ataatgtcta agtagtgac atgttttttg cacatttcc agccccctt aaatatcca cacaca

CON 360 ATAATGCTA AGTAGTGAC ATGTTTTTG CACATTTC AGCCCCCTT AAATATCCA CACACA
PCA3 1 M F L H I S S P F K Y P H T

3 158 caggaagca caaaaggaa gcacagag
4 1 a tccctggga gaaatgcc gcccgccat cttggg

CON 421 CAGGAAGCA CAAAGGAA GCACAGAGA TCCCTGGGA GAAATGCCC GGCCGCCAT CTTGGG
PCA3 15 Q E A Q K E A Q R S L G E M P G R H L G

4 tcatcgatg agcctcgcc ctgtgcctg gtcccgctt gtgAGGGAA GGACATTAG AAA
35

CON 481 TCATCGATG AGCCTCGCC CTGTGCCCTG GTCCCGCTT GTGAGGGA GGACATTAG AAA
pCA3 35 S S M S L A L C L V P L V R E G H ***

4 93 ATGAATTGAT GTGTTCCCTTA AAGGATGGC AGGAAACAG ATCCTGTTGT GGATATTAT

CON 538 ATGAATTGAT GTGTTCTCTTA AAGGATGGC AGGAAACAG ATCCTGTTGT GGATATTTAT

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APPROVED	O.G. FIG.	
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DRAFTSMAN		

00EFS0"ET20460

4 153 TTGAACGGGA TTACAGATT TAAATGAAGT CACAAAGTGA GCATTACCA TGAGAGGAAA

CON 598 TTGAACGGGA TTACAGATT TAAATGAAGT CACAAAGTGA GCATTACCA TGAGAGGAAA

4 213 ACAGACGAGA AAATCTTGAT GGCTTCACAA GACATGCAAC AAACAAAATG GAATACTGTG

CON 658 ACAGACGAGA AAATCTTGAT GGCTTCACAA GACATGCAAC AAACAAAATG GAATACTGTG

4 273 ATGACATGAG GCAGCCAAGC TGGGGaggag ataaccacgg ggcaGAGGGT CAGGATTCTG

CON 718 ATGACATGAG GCAGCCAAGC TGGGGAGGAG ATAACCACGG GGCAGAGGGT CAGGATTCTG

4 333 GCCCTGCTGC CTAAACTGTG CGTTCATAAC CAAATCATTT CATATTTCTA ACCCTCAAAA

CON 778 GCCCTGCTGC CTAAACTGTG CGTTCATAAC CAAATCATTT CATATTTCTA ACCCTCAAAA

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DEF 90" ET 20460

APPROVED	O.G. FIG.	
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4 393 CAAAGCTGTT GTAATATCTG ATCTCTACGG TTCCTTCTGG GCCCAACATT CTCCATATAT

CON 838 CAAAGCTGTT GTAATATCTG ATCTCTACGG TTCCTTCTGG GCCCAACATT CTCCATATAT

4 453 CCAGCCACAC TCATTTTAA TATTAGTTC CCAGATCTGT ACTGTGACCT TTCTACACTG

CON 898 CCAGCCACAC TCATTTTAA TATTAGTTC CCAGATCTGT ACTGTGACCT TTCTACACTG

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4 513 TAGAATAACA TTAATCATTT TGTTCAA
5 1 GA CCTTCGTGT TGCTGCCCTAA TATGTAGCTG

CON 958 TAGAATAACA TTAATCATTT TGTTCAAAGA CCTTCGTGT TGCTGCCCTAA TATGTAGCTG

5 33 ACTGTTTTTC CTAAGGAGTG TTCTGGCCCA GGGATCTGT GAACAGGCTG GGAAGCATCT

CON 1018 ACTGTTTTTC CTAAGGAGTG TTCTGGCCCA GGGATCTGT GAACAGGCTG GGAAGCATCT

5 93 CAAGATCTTT CCAGGGTTAT ACTTACTAGC ACACAGCATG ATCATTACGG AGTGAATTAT

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APPROVED	O.G. FIG.	
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CON 1078	CAAGATCTTT	CCAGGGTTAT	ACTTACTAGC	ACACAGCATG	ATCATTACCG	AGTGAATTAT
5	CTAATCAACA	TCATCCTCAG	TGTCCTTTGCC	CATACTGAAA	TTCATTTTCCC	ACTTTTGTGC
CON 1138	CTAATCAACA	TCATCCTCAG	TGTCCTTTGCC	CATACTGAAA	TTCATTTTCCC	ACTTTTGTGC
5	CCATTCTCAA	GACCTCAAAA	TGTCATTCCA	TTAATATCAC	AGGATTAACT	TTTTTTTTTTA
CON 1198	CCATTCTCAA	GACCTCAAAA	TGTCATTCCA	TTAATATCAC	AGGATTAACT	TTTTTTTTTTA
5	ACCTGGAAGA	ATTCAATGTT	ACATGCAGCT	ATGGGAAATT	AATTACATAT	TTTGTGTTTCC
CON 1258	ACCTGGAAGA	ATTCAATGTT	ACATGCAGCT	ATGGGAAATT	AATTACATAT	TTTGTGTTTCC
5	AGTGCAAAGA	TGACTAAGTC	CTTTATCCCT	CCCCCTTTGTT	TGATTTTTTTT	TCCAGTATAAA
CON 1318	AGTGCAAAGA	TGACTAAGTC	CTTTATCCCT	CCCCCTTTGTT	TGATTTTTTTT	TCCAGTATAAA

fish

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APPROVED	O.G.FIG.	
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DRAFTSMAN		

OFFICIAL RECORD

5 393 AGTTAAATG CTTAGCCTTG TACTGAGGCT GTATACAGCA CAGCCTCTCC CCATCCCCTCC
 CON 1378 AGTTAAATG CTTAGCCTTG TACTGAGGCT GTATACAGCA CAGCCTCTCC CCATCCCCTCC

 5 453 AGCCTTATCT GTCATCACCA TCAACCCCTC CCATNYSACC TAAACAAAAT CTAACCTTGTA
 CON 1438 AGCCTTATCT GTCATCACCA TCAACCCCTC CCATNYSACC TAAACAAAAT CTAACCTTGTA

 5 513 ATTCCCTTGAA CATGTCAGGN CATACTTTC TCCCTCTGCC TGAGAAGCTC TTCCTTGTCT
 CON 1498 ATTCCCTTGAA CATGTCAGGN CATACTTTC TCCCTCTGCC TGAGAAGCTC TTCCTTGTCT

 5 573 CTTAANTCTA GAATGATGTA AAGTTTGTAA TAAGTTGACT ATCTTACTTC ATGCAAAGAA
 CON 1558 CTTAANTCTA GAATGATGTA AAGTTTGTAA TAAGTTGACT ATCTTACTTC ATGCAAAGAA

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APPROVED	O.G. FIG.	
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DRAFT SHAH		

00ET90" ET 220460

5 633 GGGACACATA TGAGATTTCAT CATCACATGA GACAGCAAAT ACTAAAAGTG TAATTGATT
CON 1618 GGGACACATA TGAGATTTCAT CATCACATGA GACAGCAAAT ACTAAAAGTG TAATTGATT

5 693 ATAAGAGTTT AGATAAATAT ATGAAATGCA AGAKCCACAG AGGGAATGTT TATGGGGCAC
CON 1678 ATAAGAGTTT AGATAAATAT ATGAAATGCA AGAKCCACAG AGGGAATGTT TATGGGGCAC

5 753 GTTTGTAAGC CTGGGATGTG AAGMAAAGGC AGGGAACCTC ATAGTATCTT ATATAATATA
CON 1738 GTTTGTAAGC CTGGGATGTG AAGMAAAGGC AGGGAACCTC ATAGTATCTT ATATAATATA

5 813 CTTTCATTCT CTATCTCTAT CACAATATCC AACAAAGCTTT TCACAGAATT CATGCAGTGC
CON 1798 CTTTCATTCT CTATCTCTAT CACAATATCC AACAAAGCTTT TCACAGAATT CATGCAGTGC

5 873 AAATCCCCAA AGGTAACCTT TATCCATTTC ATGGTGAGTG CGCTTTAGAA TTTTGGCAAA

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

006790" ET 20460

WO 98/45420

09/402713
PCT/CA98/00346

CON 1858 AAATCCCCAA AGGTAACCTT TATCCATTTC ATGGTGAGTG CGCTTTAGAA TTTTGGCAAA

5 933 TCATACTGGT CACTTATCTC AACTTTGAGA TGTGTTTGTC CTTGTAGTTA ATTGAAAGAA

CON 1918 TCATACTGGT CACTTATCTC AACTTTGAGA TGTGTTTGTC CTTGTAGTTA ATTGAAAGAA

5 993 ATAGGGCACT CTTgtgagcc actttagggt tcaactcctgg caataaagaa tttacaaga

CON 1978 ATAGGGCACT CTTgtgagcc actttagggt tcaactcctgg caataaagaa tttacaaga

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APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN		

PCA3 cDNA clones

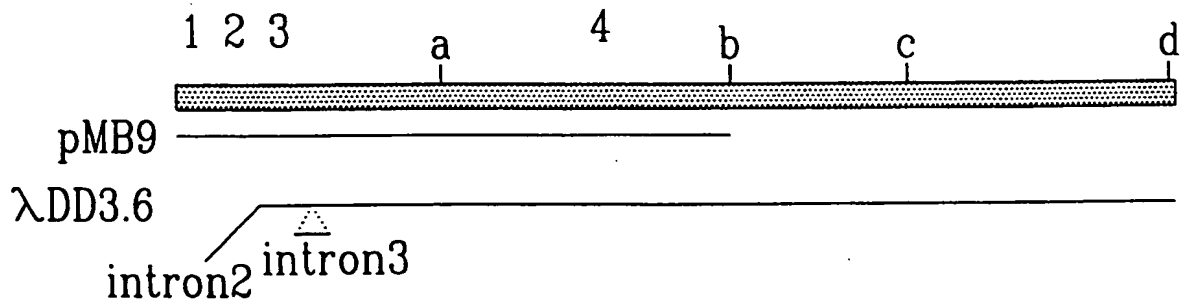
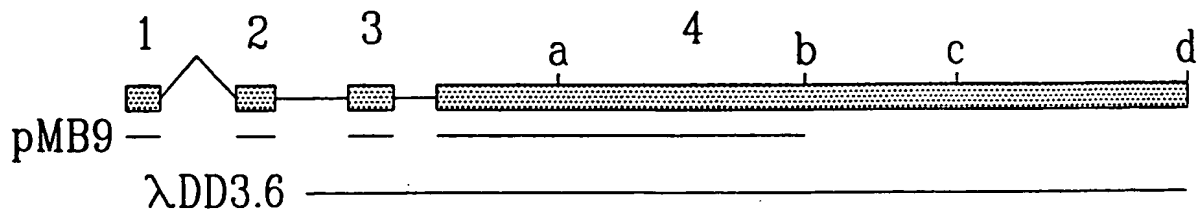


FIG. 3

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APPROVED	O.G. FIG.
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PE | S1 | 5' RACE | 5' RACE | CDNAS
▼ ▼ ▼ ▼ ▼
...g ACAGAAG AAATAGCAAG TGCCGAGAAG CTGGCATCAG
L → TSS L → pMB9
AAAAACAGAG GGGAGATTG TGTGGCTGCA GCCGAGGGAG ACCAGGAAGA
TCTGCATGGT GGGAAGGACC TGATGATACA GAG gt ...
└─ splice site

FIG. 4

APPROVED	O.G. FIG.	
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DRAFTSMAN		

00ET90" ET 20460

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286
285
121 469 1008 2067 2623
1 120 468 1007 2066 2622 3582
=====
>E1>E2>E3->-EXON-4A->-EXON-4B----->-EXON-4C->-EXON-4D----->
>PCA3>
1|-----| 3582
401 553
FIG - 5A

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Sequence PCA3 cDNA and PCA3 protein:

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1 ACAGAAGAAA TAGCAAGTGC CGAGAAGCTG GCATCAGAAA AACAGAGGGG AGATTGTGT
61 GGCTGCAGCC GAGGGAGACC AGGAAGATCT GCATGGTGGG AAGGACCTGA TGATACAGAG
121 GAATTACAAC ACATATACTT AGTGTTTCAA TGAACACCAA GATAAATAAG TGAAGAGCTA
181 GTCCGCTGTG AGTCTCCTCA GTGACACAGG GCTGGATCAC CATCGACGGC ACTTCTGAG
241 TACTCAGTGC AGCAAAGAAA GACTACAGAC ATCTCAATGG CAGGGGTGAG AAATAAGAAA
301 GGCTGCTGAC TTTACCATCT GAGGCCACAC ATCTGCTGAA ATGGAGATAA TTAACATCAC
FIG - 5B

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APPROVED	O.G. FIG.	
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DRAFTSHAH		

"SECRET" E F 20460

361 TAGAAACAGC AAGATGACAA TATAATGTCT AAGTAGTGAC **ATG**TTTTTTC ACATTTCACAG
PCA3 1 M F L H I S S

421 CCCCTTTAAA TATCCACACA CACAGGAAGC ACAAAGGAA GCACAGAGAT CCCTGGGAGA
PCA3 8 P F K Y P H T Q E A Q K E A Q R S L G E

481 AATGCCCGGC CGCCATCTTG GGTCAATCGAT GAGCCTCGCC CTGTGCCCTGG TCCCGCTTGT
PCA3 28 M P G R H L G S S M S L A L C L V P L V

541 GAGGGAAGGA CATTAGAAA TGAATTGATG TGTTCCCTTAA AGGATGGGCA GGAAACACAGA
PCA3 48 R E G H *

601 TCCTGTTGTG GATATTATT TGAACGGGAT TACAGATTG AAATGAAGTC ACAAAGTGAG

661 CATTACCAAT GAGAGGAAA CAGACGAGAA AATCTTGATG GCTTCACAAG ACATGCAACA

721 AACAAAATGG AATACTGTGA TGACATGAGG CAGCCAAGCT GGGGAGGAGA TAACCACGGG

781 GCAGAGGGTC AGGATTCTGG CCTGCTGCC TAAACTGTGC GTTCATAACC AAATCATTTT

841 ATATTCTTAA CCTCAAAAC AAAGCTGTTG TAATATCTGA TCTCTACGGT TCCTTCTGGG

901 CCCAACATTC TCCATATATC CAGCCACACT CATTTTTAAT ATTAGTTCC CAGATCTGTA

961 CTGTGACCCTT TCTACACTGT AGAATAACAT TACTCATTTT GTTCAAAGAC CCTTCGTGTT

1021 GCTGCCTAAT ATGTAGCTGA CTGTTTTTCC TAAGGAGTGT TCTGGCCCAG GGGATCTGTG

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APPROVED	O.G. FIG.	
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11081	AACAGGCTGG	GAAGCATCTC	AAGATCTTTC	CAGGGTTATA	CTTACTAGCA	CACAGCATGA
11141	TCATTACGGA	GTGAATTATC	TAATCAACAT	CATCCTCAGT	GTCTTTGCC	ATACTGAAAT
11201	TCATTTCCCA	CTTTTGTGCC	CATTCTCAAG	ACCTCAAAAT	GTCAATCCAT	TAATATCACA
11261	GGATTAACTT	TTTTTTTAA	CCTGGAAGAA	TTCAATGTTA	CATGCAGCTA	TGGGAATTTA
11321	ATTACATATT	TTGTTTTCCA	GTGCAAAAGAT	GACTAAGTCC	TTTATCCCTC	CCCTTTGTTT
11381	GATTTTTTTT	CCAGTATAAA	GTTAAAAATGC	TTAGCCTTGT	ACTGAGGCTG	TATACAGCAC
11441	AGCCTCTCCC	CATCCCTCCA	GCCTTATCTG	TCATCACCAT	CAACCCCTCC	CATACCACCT
11501	AAACAAAATC	TAACTTGTA	TTCCTTGAAC	ATGTCAGGAC	ATACATTATT	CCTTCTGCCT
11561	GAGAAAGCTCT	TCCTTGTCTC	TTAAATCTAG	AATGATGTAA	AGTTTGAAT	AAGTTGACTA
11621	TCCTTACTTCA	TGCAAGAAG	GGACACATAT	GAGATTCAATC	ATCACATGAG	ACAGCAAATA
11681	CTAAAAGTGT	AATTTGATTA	TAAGAGTTTA	GATAAATATA	TGAAATGCAA	GAGCCACAGA
11741	GGGAATGTTT	ATGGGGCACG	TTTGTAAGCC	TGGGATGTGA	AGCAAAGGCA	GGGAACCTCA
11801	TAGTATCTTA	TATAATATAC	TTCATTTTCTC	TATCTCTATC	ACAATATCCA	ACAAGCTTTT
11861	CACAGAATTC	ATGCAGTGCA	AATCCCCAAA	GGTAACCTTT	ATCCATTTC	TGGTGAGTGC

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APPROVED	O.G. FIG.	
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1921 GCTTTAGAAT TTTGGCAAAT CATACTGGTC ACTTATCTCA ACTTTGAGAT GTGTTTGTCC
 1981 TTGTAGTTAA TTGAAAGAAA TAGGGCACTC TTGTGAGCCA CTTTAGGGTT CACTCCCTGGC
 2041 AATAAAGAAT TTACAAAGAG CTACTCAGGA CCAGTTGTTA AGAGCTCTGT GTGTGTGTGT
 2101 GTGTGTGTGT GAGGTACAT GCCAAAGTGT GCCTCTCTCT CTTGACCCAT TATTTACAGAC
 2161 TTAAACAAG CATGTTTCA AATGGCACTA TGAGCTGCCA ATGATGTATC ACCACCATAT
 2221 CTCATTATTC TCCAGTAAAT GTGATAATAA TGTCATCTGT TAACATAAAA AAAGTTTGAC
 2281 TTCACAAAAG CAGCTGGAAA TGGACAACCA CAATATGCAT AAATCTAACT CCTACCATCA
 2341 GCTACACACT GCTTGACATA TATTGTTAGA AGCACCTCGC ATTTGTGGGT TCTCTTAAGC
 2401 AAAATACTTG CATTAGGTCT CAGCTGGGGC TGTCATCAG GCGGTTTGAG AAATATTCAA
 2461 TTCTCAGCAG AAGCCAGAAT TTGAATTCCC TCATCTTTTA GGAATCATTT ACCAGGTTTG
 2521 GAGAGGATTC AGACAGCTCA GGTGCTTTCA CTAATGTCTC TGAACCTCTG TCCCTCTTTG
 2581 TGTTCATGGA TAGTCCAATA AATAATGTTA TCTTTGAACT GATGCTCATA GGAGAGAATA
 2641 TAAGAACTCT GAGTGATATC AACATTAGGG ATTCAAAGAA ATATTAGATT TAAGCTCACA
 2701 CTGGTCAAAA GGAACCAAGA TACAAAGAAC TCTGAGCTGT CATCGTCCCC ATCTCTGTGA

FIG. 5E

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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SEQUENCE "E" 20450

2761 GCCACAACCA ACAGCAGGAC CCAACGCATG TCTGAGATCC TTAAATCAAG GAAACCAGTG
 2821 TCATGAGTTG AATTCTCCTA TTATGGATGC TAGCTTCTGG CCATCTCTGG CTCTCCTCTT
 2881 GACACATATT AGCTTCTAGC CTTTGCTTCC ACGACTTTTA TCTTTTCTCC AACACATCGC
 2941 TTACCAATCC TCTCTCTGCT CTGTTGCTTT GGACTTCCCC ACAAGAATT CAACGACTCT
 3001 CAAGTCTTTT CTTCATCCC CACCATAAC CTGAATTGCC TAGACCCTTA TTTTATTAA
 3061 TTTCCAATAG ATGCTGCCCTA TGGGCTAATA TTGCTTTAGA TGAACATTAG ATATTTAAAG
 3121 TCTAAGAGGT TCAAAATCCA ACTCATATC TTCTCTTTCT TTCACCTCCC CTGCTCCTCT
 3181 CCTATATTA CTGATTGACT GAACAGGATG GTCCCCAAGA TGCCAGTCAA ATGAGAAACC
 3241 CAGTGGCTCC TTGTGGATCA TGCATGCAAG ACTGCTGAAG CCAGAGGATG ACTGATTACG
 3301 CCTCATGGT GGAGGGGACC ACTCCTGGGC CTTCTGTGATT GTCAGGAGCA AGACCTGAGA
 3361 TGCTCCCTGC CTTCAGTGTC CTCTGCATCT CCCCTTTCTA ATGAAGATCC ATAGAATTG
 3421 CTACATTGA GAATCCAAT TAGGAACTCA CATGTTTTAT CTGCCCTATC AATTTTTAA
 3481 ACTTGCTGAA AATTAAGTTT TTTCAAATC TGTCCTTGTA AATTACTTT TCTTACAGTG
 3541 TCTTGGCATA CTATATCAAC TTTGATTCTT TGTACAAC TT

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